

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/922,449

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ Wrapped Nucleics  
Wrapped Aminos  
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length  
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino  
Numbering  
The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☒ Non-ASCII  
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length.  
Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0  
"bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences  
(OLD RULES)  
Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences  
(NEW RULES)  
Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 ☐ Use of n's or Xaa's  
(NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213>  
Response  
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220>  
Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0  
"bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n  
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

PAGE: 1

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/922,449

DATE: 10/02/2001  
TIME: 16:21:47

Input Set: I922449.RAW

This Raw Listing contains the General  
Information Section and those Sequences  
containing ERRORS.

*see item 4  
on Error  
summary sheet*

1 <110> BioInside Gesellschaft fr Biodiagnostik, Auftragsforschung und Consulting  
2 mbH  
3 <120> Test kit and method for quantitatively detecting genetically modified DNA  
4 in foodstuff by means of  
5 fluorescence-coupled PCR  
6 <130> PCT/EP00/  
7 <140> US/09/922,449  
8 <141> 2001-08-03  
9 <150> DE 199 06 169,6  
10 <151> 1999-02-08  
11 <160> 25 OK, but see p. 3  
12 <170> PatentIn Ver. 2.1

Does Not Comply  
Corrected Diskette Needed

ERRORED SEQUENCES FOLLOW

13 <210> 1  
E--> 14 <211> 240  
15 <212> DNA  
16 <213> Artificial sequence  
17 <220>  
18 <223> Description of artificial sequence: Roundup soy gene (RRS gene)  
19 <400> 1  
20 gtcttcaaag caagtggatt gatgtgatat ctccactgac gtaagggatg acgcacaatc 60  
E--> 21 ccactatcct tcgcaagacc cttcctctat ataaggaagt tcatttcatt tggagaggac  
W--> 22 120  
E--> 23 acgctgacaa gctgactcta gcagatcttt caagaatgac acaaattaac aacatggctc  
W--> 24 180  
E--> 25 aagggaatac aacccttaac cccaattcca attccataa accccaagtt cctaaatctt  
W--> 26 240  
*see item 1 on Error summary sheet*  
*120*  
*180*  
*240*

27 <210> 8  
E--> 28 <211> 142  
29 <212> DNA  
30 <213> Artificial sequence  
31 <220>  
32 <223> Description of artificial sequence: target IAC DNA for the RRS gene  
33 <400> 8  
E--> 34 catttggaga ggacacgctg aggacgttcg ccaattttcg cctcccacgt ctcaccgagc 60  
W--> 35  
E--> 36 cgaaggtttt acgttttccc  
W--> 37  
E--> 38 tcgttttcat ccagtcctttc 120  
*see p. 4*

PAGE: 2

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/922,449

DATE: 10/02/2001  
TIME: 16:21:47

Input Set: I922449.RAW

39 atggctcaag ggatacaaac cc 142

E--> 40 <210> 8a  
E--> 41 <211> 143  
42 <212> DNA  
43 <213> Artificial sequence  
44 <220>  
45 <223> Description of artificial sequence: target IAC DNA for the RRS gene  
46 <400> 8a  
E--> 47 ctgacgtaag ggatgacgca cggacgttcg ccaattttcg cctccccacgt ctcaccgagc 60  
W--> 48  
E--> 49 cgaagggtttt acgtttttccc  
W--> 50  
E--> 51 tcgtttttcat ccagtctttt 120  
52 acaagctgac tctagcagat ctt 143

*see pp 3 & 4 (same error)*

53 <210> 10  
E--> 54 <211> 150  
55 <212> DNA  
56 <213> Artificial sequence  
57 <220>  
58 <223> Description of artificial sequence: reference IAC DNA for the RRS gene  
59 <400> 10  
E--> 60 gccctctact ccacccccat ccggacgttc gccaattttc gcctccccacg tctcaccgag 60  
W--> 61  
E--> 62 acgaagggttt tacgtttttcc  
W--> 63  
E--> 64 ttcgttttca tccagtctttt 120  
65 gacaatcggc ttgcagatgg gcttgcccttc 150

*see pp 3 & 4*

66 <210> 11  
E--> 67 <211> 250  
68 <212> DNA  
69 <213> Artificial sequence  
70 <220>  
71 <223> Description of artificial sequence: lectin gene  
72 <400> 11  
E--> 73 gggaaggtta caactcaata aggttgacga aaacggcacc ccaaaaccct cgtctcttgg 60  
W--> 74  
E--> 75 tactccaccc ccattccacat  
W--> 76  
E--> 77 gaaaccggta gcgttgccag 120 cttcgccgct tccttcaact tcaccttcta tgccccagac  
W--> 78  
E--> 79 ttgcagatgg 180 gcttgcccttc  
W--> 80  
E--> 81 caattgacac taagccacaa acacatgcag gttatcttgg 240  
82 tcttttcaac 250

*pp 3 & 4*

This needs to be  
changed to 3

09/92 449 3

<210> 2a  
<211> 24  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Description of artificial sequence: probe  
<400> 2a 3  
cccactatcc ttcgcaagac ctt

invalid - Per 1.821 of Sequence Rules,

"Each sequence  
set forth in the  
'Sequence Listings' shall  
be

assigned  
a separate  
sequence  
identifier.

The sequence  
identifiers shall  
begin with 1  
and increase  
sequentially by  
integers."

The types of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.

009224494

<210> 8  
<211> 142  
<212> DNA  
<213> Artificial sequence

<220>

<223> Description of artificial sequence: target IAC DNA for the RRS gene

<400> 8

catttggaga ggacacgctg aggacgttcg ccaattttcg cctcccacgt ctcaccgagc 60 gtggtgttta

cgaagggtttt acgttttccc gtatccctt

~~tcgttttcat ccagtcttcc 120~~

atggctcaag ggatacaaac cc

142

insert a  
hard  
return

These format errors exist  
throughout submitted file.

Input Set: I922449.RAW

Line	Error/Warning	Original Text
14	E Input 240, Calc# Bases 60 differ	<211> 240
21	E Wrong Amino Acid Designator	ccactatcct tcgcaagacc cttcctctat ataaggaa
21	E Wrong Amino Acid Designator	ccactatcct tcgcaagacc cttcctctat ataaggaa
21	E Wrong Amino Acid Designator	ccactatcct tcgcaagacc cttcctctat ataaggaa
21	E Wrong Amino Acid Designator	ccactatcct tcgcaagacc cttcctctat ataaggaa
21	E Wrong Amino Acid Designator	ccactatcct tcgcaagacc cttcctctat ataaggaa
21	E Wrong Amino Acid Designator	ccactatcct tcgcaagacc cttcctctat ataaggaa
22	W Invalid/Missing Amino Acid Numbering	120
23	E Wrong Amino Acid Designator	acgctgacaa gctgactcta gcagatcttt caagaatg
23	E Wrong Amino Acid Designator	acgctgacaa gctgactcta gcagatcttt caagaatg
23	E Wrong Amino Acid Designator	acgctgacaa gctgactcta gcagatcttt caagaatg
23	E Wrong Amino Acid Designator	acgctgacaa gctgactcta gcagatcttt caagaatg
23	E Wrong Amino Acid Designator	acgctgacaa gctgactcta gcagatcttt caagaatg
23	E Wrong Amino Acid Designator	acgctgacaa gctgactcta gcagatcttt caagaatg
24	W Invalid/Missing Amino Acid Numbering	180
25	E Wrong Amino Acid Designator	aaggataca aacccttaat cccaattcca atttccat
25	E Wrong Amino Acid Designator	aaggataca aacccttaat cccaattcca atttccat
25	E Wrong Amino Acid Designator	aaggataca aacccttaat cccaattcca atttccat
25	E Wrong Amino Acid Designator	aaggataca aacccttaat cccaattcca atttccat
25	E Wrong Amino Acid Designator	aaggataca aacccttaat cccaattcca atttccat
25	E Wrong Amino Acid Designator	aaggataca aacccttaat cccaattcca atttccat
26	W Invalid/Missing Amino Acid Numbering	240
28	E Input 142, Calc# Bases 42 differ	<211> 142
34	E Wrong Amino Acid Designator	catttgagga ggacacgctg aggacgttcg ccaatttt
34	E Wrong Amino Acid Designator	catttgagga ggacacgctg aggacgttcg ccaatttt
34	E Wrong Amino Acid Designator	catttgagga ggacacgctg aggacgttcg ccaatttt
34	E Wrong Amino Acid Designator	catttgagga ggacacgctg aggacgttcg ccaatttt
34	E Wrong Amino Acid Designator	catttgagga ggacacgctg aggacgttcg ccaatttt
34	E Wrong Amino Acid Designator	catttgagga ggacacgctg aggacgttcg ccaatttt
35	W Invalid/Missing Amino Acid Numbering	
36	E Wrong Amino Acid Designator	cgaagggtttt acgtttttccc gtatccccctt
36	E Wrong Amino Acid Designator	cgaagggtttt acgtttttccc gtatccccctt
36	E Wrong Amino Acid Designator	cgaagggtttt acgtttttccc gtatccccctt
37	W Invalid/Missing Amino Acid Numbering	
38	E Number of Bases conflict w/ Running Total	tcgttttcat ccagtctttc 120
40	E Wrong Sequence Number 8	<210> 8a
41	E Input 143, Calc# Bases 43 differ	<211> 143
47	E Wrong Amino Acid Designator	ctgacgtaag ggatgacgca cggacgttcg ccaatttt
47	E Wrong Amino Acid Designator	ctgacgtaag ggatgacgca cggacgttcg ccaatttt
47	E Wrong Amino Acid Designator	ctgacgtaag ggatgacgca cggacgttcg ccaatttt
47	E Wrong Amino Acid Designator	ctgacgtaag ggatgacgca cggacgttcg ccaatttt
47	E Wrong Amino Acid Designator	ctgacgtaag ggatgacgca cggacgttcg ccaatttt
47	E Wrong Amino Acid Designator	ctgacgtaag ggatgacgca cggacgttcg ccaatttt
48	W Invalid/Missing Amino Acid Numbering	
49	E Wrong Amino Acid Designator	cgaagggtttt acgtttttccc gtatccccctt
49	E Wrong Amino Acid Designator	cgaagggtttt acgtttttccc gtatccccctt
49	E Wrong Amino Acid Designator	cgaagggtttt acgtttttccc gtatccccctt
50	W Invalid/Missing Amino Acid Numbering	

Input Set: I922449.RAW

Line ? Error/Warning

Original Text

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51 E Number of Bases conflict w/ Running Total tcgttttcat ccagtctttg 120
54 E Input 150, Calc# Bases 50 differ <211> 150
60 E Wrong Amino Acid Designator gccctctact ccacccccat ccggacgttc gccaatth
60 E Wrong Amino Acid Designator gccctctact ccacccccat ccggacgttc gccaatth
60 E Wrong Amino Acid Designator gccctctact ccacccccat ccggacgttc gccaatth
60 E Wrong Amino Acid Designator gccctctact ccacccccat ccggacgttc gccaatth
60 E Wrong Amino Acid Designator gccctctact ccacccccat ccggacgttc gccaatth
60 E Wrong Amino Acid Designator gccctctact ccacccccat ccggacgttc gccaatth
60 E Wrong Amino Acid Designator gccctctact ccacccccat ccggacgttc gccaatth
61 W Invalid/Missing Amino Acid Numbering
62 E Wrong Amino Acid Designator acgaagggtt tacgttttcc cgtatcccct
62 E Wrong Amino Acid Designator acgaagggtt tacgttttcc cgtatcccct
62 E Wrong Amino Acid Designator acgaagggtt tacgttttcc cgtatcccct
63 W Invalid/Missing Amino Acid Numbering
64 E Number of Bases conflict w/ Running Total ttcgttttca tccagtcttt 120
67 E Input 250, Calc# Bases 50 differ <211> 250
73 E Wrong Amino Acid Designator gggaaagtta caactcaata aggttgacga aaacggca
73 E Wrong Amino Acid Designator gggaaagtta caactcaata aggttgacga aaacggca
73 E Wrong Amino Acid Designator gggaaagtta caactcaata aggttgacga aaacggca
73 E Wrong Amino Acid Designator gggaaagtta caactcaata aggttgacga aaacggca
73 E Wrong Amino Acid Designator gggaaagtta caactcaata aggttgacga aaacggca
73 E Wrong Amino Acid Designator gggaaagtta caactcaata aggttgacga aaacggca
73 E Wrong Amino Acid Designator gggaaagtta caactcaata aggttgacga aaacggca
74 W Invalid/Missing Amino Acid Numbering
75 E Wrong Amino Acid Designator tactccaccc ccattccacat ttgggacaaa
75 E Wrong Amino Acid Designator tactccaccc ccattccacat ttgggacaaa
75 E Wrong Amino Acid Designator tactccaccc ccattccacat ttgggacaaa
76 W Invalid/Missing Amino Acid Numbering
77 E Wrong Amino Acid Designator gaaaccggta gcgttgccag 120 cttcgccgct tcct
77 E Wrong Amino Acid Designator gaaaccggta gcgttgccag 120 cttcgccgct tcct
77 E Wrong Amino Acid Designator gaaaccggta gcgttgccag 120 cttcgccgct tcct
77 E Wrong Amino Acid Designator gaaaccggta gcgttgccag 120 cttcgccgct tcct
77 E Wrong Amino Acid Designator gaaaccggta gcgttgccag 120 cttcgccgct tcct
77 E Wrong Amino Acid Designator gaaaccggta gcgttgccag 120 cttcgccgct tcct
77 E Wrong Amino Acid Designator gaaaccggta gcgttgccag 120 cttcgccgct tcct
78 W Invalid/Missing Amino Acid Numbering
79 E Wrong Amino Acid Designator ttgcagatgg 180 gcttgccctt tttctcgac
79 E Wrong Amino Acid Designator ttgcagatgg 180 gcttgccctt tttctcgac
79 E Wrong Amino Acid Designator ttgcagatgg 180 gcttgccctt tttctcgac
80 W Invalid/Missing Amino Acid Numbering
81 E Number of Bases conflict w/ Running Total caattgacac taagccacaa acacatgcag gttatctt

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